SUB B1 CONT. AB

obtaining a second nucleic acid sample by fragmenting said first nucleic acid sample to produce fragments, ligating adaptor sequences to said fragments, amplifying at least some of said fragments, and isolating said amplified fragments;

providing a nucleic acid array;

hybridizing said second nucleic acid sample to said array; and

analyzing a hybridization pattern resulting from said hybridization.

40. (New) The method of claim 39 wherein said second nucleic acid sample comprises at least 0.5 % of said first nucleic acid sample.

41. (New) The method of claim 39 wherein said second nucleic acid sample comprises at least 3 % of said first nucleic acid sample.

SUB C1

42. (New) The method of claim 39 wherein said second nucleic acid sample comprises at least 12 % of said first nucleic acid sample.

43. (New) The method of claim 39 wherein said second nucleic acid sample comprises at least 50 % of said first nucleic acid sample.

44. (New) The method of claim 39 wherein said first nucleic acid sample is DNA.

45. (New) The method of claim 39 wherein said first nucleic acid sample is genomic DNA.

46. (New) The method of claim 39 wherein said first nucleic acid sample is cDNA derived from RNA or mRNA.

47. (New) The method of claim 39 wherein the entire method is performed in a single reaction vessel.

48. (New) The method of claim 39 wherein said step of fragmenting the first nucleic acid sample comprises digestion with at least one restriction enzyme.

49. (New) The method of claim 39 wherein said step of fragmenting the first nucleic acid sample comprises digestion with a type IIs endonuclease.

50. (New) The method of claim 39 wherein said adaptor sequences comprise PCR primer template sequences.

51. (New) The method of claim 39 wherein said adaptor sequences comprise tag sequences.

52. (New) The method of claim 39 wherein said method for analyzing a first nucleic acid sample comprises determining whether the first nucleic acid sample contains sequence variations.

53. (New) The method of claim 52 wherein said sequence variations are single nucleotide polymorphisms (SNPs).

54. (New) The method of claim 39 wherein the nucleic acid array is designed to query DNA fragments which have been produced by the identical procedures used to obtain said second nucleic acid sample.

55. (New) The method of claim 54 wherein the sequences contained in said second nucleic acid sample are predetermined.

56. (New) The method of claim 54 wherein said sequences contained in said second nucleic acid sample are first determined by a computer system.

57. (New) The method of claim 53 wherein said second nucleic acid sample is obtainable by:

binding oligonucleotide probes containing a desired SNP sequence to magnetic beads to form probe-bead complexes;

hybridizing said probe-bead complexes to said first nucleic acid sample;

exposing said first nucleic acid sample to a single strand DNA nuclease to remove single stranded DNA thereby obtaining only DNA duplexes;

ligating a double stranded adaptor sequence comprising a restriction enzyme site to said DNA duplexes;

digesting said DNA duplexes with a restriction enzyme to release the magnetic bead; and

isolating the duplexes.

58. (New) The method of claim 57 wherein said restriction enzyme is a Class IIs endonuclease.

59. (New) The method of claim 53 wherein said second nucleic acid sample is obtainable by:

exposing the first nucleic acid sample to a mismatch binding protein;

employing a 3' to 5' exonuclease to remove one strand of double stranded DNA; and

employing a nuclease to remove single stranded DNA.

60. (New) A method of screening for DNA sequence variations in an individual comprising:

providing a first nucleic acid sample from said individual;

obtaining a second nucleic acid sample by fragmenting said first nucleic acid sample to produce fragments, ligating adaptor sequences to said fragments, amplifying at least some of said fragments, and isolating said amplified fragments;

providing a nucleic acid array wherein said array comprises probes designed to interrogate for DNA sequence variations;

hybridizing said second nucleic acid sample to said array;

generating a hybridization pattern resulting from said hybridization; and

determining the presence or absence of DNA sequence variations in the individual based upon an analysis of the hybridization pattern.

61. (New) The method of claim 60 wherein said sequence variation is a single nucleotide polymorphism (SNP).

62. (New) The method of claim 61 wherein said SNP is associated with a disease.

63. (New) The method of claim 61 wherein said SNP is associated with the efficacy of a drug.

64. (New) A method of analyzing a first nucleic acid sample comprising:

providing said first nucleic acid sample;

obtaining a second nucleic acid sample by fragmenting said first nucleic acid sample to produce fragments, denaturing said fragments, allowing at least some of said fragments to reanneal to form double stranded DNA sequences and removing said double stranded DNA sequences thus isolating said single stranded fragments;

providing a nucleic acid array;

hybridizing said second nucleic acid sample to said array; and

analyzing a hybridization pattern resulting from said hybridization.

65. (New) The method of claim 64 further comprising the step of amplifying the isolated fragments.

66. (New) The method of claim 64 wherein said step of amplifying is performed by a polymerase chain reaction (PCR).

67. (New) The method of claim 64 wherein said second nucleic acid sample comprises at least 0.5 % of said first nucleic acid sample.

68. (New) The method of claim 64 wherein said second nucleic acid sample comprises at least 3 % of said first nucleic acid sample.

69. (New) The method of claim 64 wherein said second nucleic acid sample comprises at least 12 % of said first nucleic acid sample.

70. (New) The method of claim 64 wherein said second nucleic acid sample comprises at least 50 % of said first nucleic acid sample.

71. (New) The method of claim 64 wherein said first nucleic acid sample is DNA.

72. (New) The method of claim 64 wherein said first nucleic acid sample is genomic DNA.

73. (New) The method of claim 64 wherein said first nucleic acid sample is cDNA derived from RNA or mRNA.

74. (New) The method of claim 64 wherein the entire method is performed in a single reaction vessel.

75. (New) The method of claim 64 wherein said step of fragmenting the first nucleic acid sample comprises digestion with at least one restriction enzyme.

76. (New) The method of claim 64 wherein said step of fragmenting the first nucleic acid sample comprises digestion with a type IIs endonuclease.

77. (New) The method of claim 64 wherein said method for analyzing a first nucleic acid sample comprises determining whether the first nucleic acid sample contains sequence variations.

78. (New) The method of claim 77 wherein said sequence variations are single nucleotide polymorphisms (SNPs).

79. (New) The method of claim 64 wherein the nucleic acid array is designed to query DNA fragments which have been produced by the identical procedures used to obtain said second nucleic acid sample.

80. (New) The method of claim 79 wherein the sequences contained in said second nucleic acid sample are predetermined.

81. (New) The method of claim 79 wherein said sequences contained in said second nucleic acid sample are first determined by a computer system.

A13

82. (New) The method of claim 78 wherein said second nucleic acid sample is obtainable by:

binding oligonucleotide probes containing a desired SNP sequence to magnetic beads to form probe-bead complexes;

hybridizing said probe-bead complexes to said first nucleic acid sample;

exposing said first nucleic acid sample to a single strand DNA nuclease to remove single stranded DNA thereby obtaining only DNA duplexes;

ligating a double stranded adaptor sequence comprising a restriction enzyme site to said DNA duplexes;

digesting said DNA duplexes with a restriction enzyme to release the magnetic bead; and

isolating the duplexes.

83. (New) The method of claim 82 wherein said restriction enzyme is a Class IIs endonuclease.

84. (New) The method of claim 78 wherein said second nucleic acid sample is obtainable by:

exposing the first nucleic acid sample to a mismatch binding protein;

employing a 3' to 5' exonuclease to remove one strand of double stranded DNA; and

employing a nuclease to remove single stranded DNA.

85. (New) A method of screening for DNA sequence variations in an individual comprising:

providing a first nucleic acid sample from said individual;

obtaining a second nucleic acid sample by fragmenting said first nucleic acid sample to produce fragments, denaturing said fragments, allowing some of said

fragments to reanneal to form double stranded DNA sequences and removing said double stranded DNA sequences thus isolating said single stranded fragments;

providing a nucleic acid array wherein said array comprises probes designed to interrogate for DNA sequence variations;

hybridizing said second nucleic acid sample to said array;

generating a hybridization pattern resulting from said hybridization; and

determining the presence or absence of DNA sequence variations in the individual based upon an analysis of the hybridization pattern.

86. (New) The method of claim 85 wherein said sequence variation is a single nucleotide polymorphism (SNP).

87. (New) The method of claim 86 wherein said SNP is associated with a disease.

88. (New) The method of claim 86 wherein said SNP is associated with the efficacy of a drug.

89. (New) A method of analyzing a first nucleic acid sample comprising:

providing said first nucleic acid sample;

obtaining a second nucleic acid sample by amplifying said first nucleic acid sample by arbitrarily primed PCR to produce an amplification product and isolating said amplification product;

providing a nucleic acid array;

hybridizing said second nucleic acid sample to said array; and

analyzing a hybridization pattern resulting from said hybridization.

90. (New) The method of claim 89 wherein said second nucleic acid sample comprises at least 0.5 % of said first nucleic acid sample.

91. (New) The method of claim 89 wherein said second nucleic acid sample comprises at least 3 % of said first nucleic acid sample.

92. (New) The method of claim 89 wherein said second nucleic acid sample comprises at least 12 % of said first nucleic acid sample.

93. (New) The method of claim 89 wherein said second nucleic acid sample comprises at least 50 % of said first nucleic acid sample.

94. (New) The method of claim 89 wherein said first nucleic acid sample is DNA.

95. (New) The method of claim 89 wherein said first nucleic acid sample is genomic DNA.

96. (New) The method of claim 89 wherein said first nucleic acid sample is cDNA derived from RNA or mRNA.

97. (New) The method of claim 89 wherein the entire method is performed in a single reaction vessel.

98. (New) The method of claim 89 wherein said step of fragmenting the first nucleic acid sample comprises digestion with at least one restriction enzyme.

99. (New) The method of claim 89 wherein said step of fragmenting the first nucleic acid sample comprises digestion with a type IIs endonuclease.

100. (New) The method of claim 89 wherein said method for analyzing a first nucleic acid sample comprises determining whether the first nucleic acid sample contains sequence variations.

101. (New) The method of claim 100 wherein said sequence variations are single nucleotide polymorphisms (SNPs).

102. (New) The method of claim 89 wherein the nucleic acid array is designed to query DNA fragments which have been produced by the identical procedures used to obtain said second nucleic acid sample.

103. (New) The method of claim 102 wherein the sequences contained in said second nucleic acid sample are predetermined.

104. (New) The method of claim 102 wherein said sequences contained in said second nucleic acid sample are first determined by a computer system.

105. (New) The method of claim 101 wherein said second nucleic acid sample is obtainable by:

binding oligonucleotide probes containing a desired SNP sequence to magnetic beads to form probe-bead complexes;

hybridizing said probe-bead complexes to said first nucleic acid sample;

exposing said first nucleic acid sample to a single strand DNA nuclease to remove single stranded DNA thereby obtaining only DNA duplexes;

ligating a double stranded adaptor sequence comprising a restriction enzyme site to said DNA duplexes;

digesting said DNA duplexes with a restriction enzyme to release the magnetic bead; and

isolating the duplexes.

106. (New) The method of claim 105 wherein said restriction enzyme is a Class IIs endonuclease.

107. (New) The method of claim 101 wherein said second nucleic acid sample is obtainable by:

exposing the first nucleic acid sample to a mismatch binding protein;

employing a 3' to 5' exonuclease to remove one strand of double stranded DNA; and

employing a nuclease to remove single stranded DNA.

108. (New) A method of screening for DNA sequence variations in an individual comprising:

providing a first nucleic acid sample from said individual;

obtaining a second nucleic acid sample by amplifying said first nucleic acid sample by arbitrarily primed PCR to produce an amplification product and isolating said amplification product ;

providing a nucleic acid array wherein said array comprises probes designed to interrogate for DNA sequence variations;

hybridizing said second nucleic acid sample to said array;

generating a hybridization pattern resulting from said hybridization; and

determining the presence or absence of DNA sequence variations in the individual based upon an analysis of the hybridization pattern.

109. (New) The method of claim 108 wherein said sequence variation is a single nucleotide polymorphism (SNP).

110. (New)The method of claim 109 wherein said SNP is associated with a disease.

111. (New) The method of claim 109 wherein said SNP is associated with the efficacy of a drug.

112. (New) A method of analyzing a first nucleic acid sample comprising:

providing said first nucleic acid sample;

obtaining a second nucleic acid sample by fragmenting said first nucleic acid sample to produce fragments, hybridizing said fragments to an oligonucleotide probe bound to a solid support, and isolating said hybridized fragments;

providing a nucleic acid array;

hybridizing said second nucleic acid sample to said array; and

analyzing a hybridization pattern resulting from said hybridization.

113. (New) The method of claim 112 further comprising the step of amplifying the isolated fragments.

114. (New) The method of claim 112 wherein said step of amplifying is performed by a polymerase chain reaction (PCR).

115. (New) The method of claim 112 wherein said second nucleic acid sample comprises at least 0.5 % of said first nucleic acid sample.

A13

116. (New) The method of claim 112 wherein said second nucleic acid sample comprises at least 3 % of said first nucleic acid sample.

117. (New) The method of claim 112 wherein said second nucleic acid sample comprises at least 12 % of said first nucleic acid sample.

118. (New) The method of claim 112 wherein said second nucleic acid sample comprises at least 50 % of said first nucleic acid sample.

119. (New) The method of claim 112 wherein said first nucleic acid sample is DNA.

120. (New) The method of claim 112 wherein said first nucleic acid sample is genomic DNA.

121. (New) The method of claim 112 wherein said first nucleic acid sample is cDNA derived from RNA or mRNA.

122. (New) The method of claim 112 wherein the entire method is performed in a single reaction vessel.

123. (New) The method of claim 112 wherein said step of fragmenting the first nucleic acid sample comprises digestion with at least one restriction enzyme.

124. (New) The method of claim 112 wherein said step of fragmenting the first nucleic acid sample comprises digestion with a type IIs endonuclease.

125. (New) The method of claim 112 wherein said solid support is a magnetic bead.

126. (New) The method of claim 112 wherein said method for analyzing a first nucleic acid sample comprises determining whether the first nucleic acid sample contains sequence variations.

127. (New) The method of claim 126 wherein said sequence variations are single nucleotide polymorphisms (SNPs).

128. (New) The method of claim 112 wherein the nucleic acid array is designed to query DNA fragments which have been produced by the identical procedures used to obtain said second nucleic acid sample.

129. (New) The method of claim 128 wherein the sequences contained in said second nucleic acid sample are predetermined.

130. (New) The method of claim 128 wherein said sequences contained in said second nucleic acid sample are first determined by a computer system.

131. (New) The method of claim 127 wherein said second nucleic acid sample is obtainable by:

binding oligonucleotide probes containing a desired SNP sequence to magnetic beads to form probe-bead complexes;

hybridizing said probe-bead complexes to said first nucleic acid sample;

exposing said first nucleic acid sample to a single strand DNA nuclease to remove single stranded DNA thereby obtaining only DNA duplexes;

ligating a double stranded adaptor sequence comprising a restriction enzyme site to said DNA duplexes;

digesting said DNA duplexes with a restriction enzyme to release the magnetic bead; and

isolating the duplexes.

AB

132. (New) The method of claim 131 wherein said restriction enzyme is a Class IIs endonuclease.

133. (New) The method of claim 127 wherein said second nucleic acid sample is obtainable by:

exposing the first nucleic acid sample to a mismatch binding protein;

employing a 3' to 5' exonuclease to remove one strand of double stranded DNA; and

employing a nuclease to remove single stranded DNA.

134. (New) A method of screening for DNA sequence variations in an individual comprising:

providing a first nucleic acid sample from said individual;

obtaining a second nucleic acid sample by fragmenting said first nucleic acid sample to produce fragments, hybridizing said fragments to an oligonucleotide probe bound to a solid support, and isolating said hybridized fragments;

providing a nucleic acid array wherein said array comprises probes designed to interrogate for DNA sequence variations;

hybridizing said second nucleic acid sample to said array;

generating a hybridization pattern resulting from said hybridization; and

determining the presence or absence of DNA sequence variations in the individual based upon an analysis of the hybridization pattern.

135. (New) The method of claim 134 wherein said sequence variation is a single nucleotide polymorphism (SNP).

136. (New) The method of claim 135 wherein said SNP is associated with a disease.

137. (New) The method of claim 135 wherein said SNP is associated with the efficacy of a drug.

138. (New) A method of analyzing a first nucleic acid sample comprising:

providing said first nucleic acid sample;

obtaining a second nucleic acid sample by fragmenting said first nucleic acid sample to produce fragments, binding said fragments to a mismatch binding protein, and isolating said bound fragments;

providing a nucleic acid array;

hybridizing said second nucleic acid sample to said array; and

analyzing a hybridization pattern resulting from said hybridization..

139. (New) The method of claim 138 further comprising the step of amplifying the isolated fragments.

140. (New) The method of claim 138 wherein said step of amplifying is performed by a polymerase chain reaction (PCR).

141. (New) The method of claim 138 wherein said second nucleic acid sample comprises at least 0.5 % of said first nucleic acid sample.

142. (New) The method of claim 138 wherein said second nucleic acid sample comprises at least 3 % of said first nucleic acid sample.

143. (New) The method of claim 138 wherein said second nucleic acid sample comprises at least 12 % of said first nucleic acid sample.

144. (New) The method of claim 138 wherein said second nucleic acid sample comprises at least 50 % of said first nucleic acid sample.

145. (New) The method of claim 138 wherein said first nucleic acid sample is DNA.

146. (New) The method of claim 138 wherein said first nucleic acid sample is genomic DNA.

147. (New) The method of claim 138 wherein said first nucleic acid sample is cDNA derived from RNA or mRNA.

148. (New) The method of claim 138 wherein the entire method is performed in a single reaction vessel.

149. (New) The method of claim 138 wherein said step of fragmenting the first nucleic acid sample comprises digestion with at least one restriction enzyme.

150. (New) The method of claim 138 wherein said step of fragmenting the first nucleic acid sample comprises digestion with a type IIs endonuclease.

151. (New) The method of claim 138 wherein said mismatch binding protein is bound to a magnetic bead.

152. (New) The method of claim 138 wherein said method for analyzing a first nucleic acid sample comprises determining whether the first nucleic acid sample contains sequence variations.

153. (New) The method of claim 152 wherein said sequence variations are single nucleotide polymorphisms (SNPs).

154. (New) The method of claim 138 wherein the nucleic acid array is designed to query DNA fragments which have been produced by the identical procedures used to obtain said second nucleic acid sample.

155. (New) The method of claim 154 wherein the sequences contained in said second nucleic acid sample are predetermined.

156. (New) The method of claim 154 wherein said sequences contained in said second nucleic acid sample are first determined by a computer system.

A13

157. (New) The method of claim 153 wherein said second nucleic acid sample is obtainable by:

binding oligonucleotide probes containing a desired SNP sequence to magnetic beads to form probe-bead complexes;

hybridizing said probe-bead complexes to said first nucleic acid sample;

exposing said first nucleic acid sample to a single strand DNA nuclease to remove single stranded DNA thereby obtaining only DNA duplexes;

ligating a double stranded adaptor sequence comprising a restriction enzyme site to said DNA duplexes;

digesting said DNA duplexes with a restriction enzyme to release the magnetic bead; and

isolating the duplexes.

158. (New) The method of claim 157 wherein said restriction enzyme is a Class IIs endonuclease.

159. (New) The method of claim 153 wherein said second nucleic acid sample is obtainable by:

exposing the first nucleic acid sample to a mismatch binding protein;

employing a 3' to 5' exonuclease to remove one strand of double stranded DNA; and

employing a nuclease to remove single stranded DNA.

160. (New) A method of screening for DNA sequence variations in an individual comprising:

providing a first nucleic acid sample from said individual;

obtaining a second nucleic acid sample by fragmenting said first nucleic acid sample to produce fragments, binding said fragments to a mismatch binding protein, and isolating said bound fragments;

providing a nucleic acid array wherein said array comprises probes designed to interrogate for DNA sequence variations;

hybridizing said second nucleic acid sample to said array;

A13

generating a hybridization pattern resulting from said hybridization; and

determining the presence or absence of DNA sequence variations in the individual based upon an analysis of the hybridization pattern.

161. (New) The method of claim 160 wherein said sequence variation is a single nucleotide polymorphism (SNP).

162. (New) The method of claim 161 wherein said SNP is associated with a disease.

163. (New) The method of claim 161 wherein said SNP is associated with the efficacy of a drug.

164. (New) A method of screening for DNA sequence variations in a population of individuals comprising:

providing a first nucleic acid sample from each of said individuals;

providing a second nucleic acid sample by fragmenting said first nucleic acid sample to produce fragments, ligating adaptor sequences to said fragments, amplifying at least some of said fragments, and isolating said amplified fragments;

providing a plurality of identical nucleic acid arrays wherein said arrays comprise probes which are designed to interrogate for DNA sequence variations;

hybridizing each of said second nucleic acid samples to one of said plurality of identical arrays; and

generating a plurality of hybridization patterns resulting from said hybridizations; and

analyzing the hybridization patterns to determine the presence or absence of sequence variation in the population of individuals.

165. (New) The method of claim 164 wherein said sequence variation is a single nucleotide polymorphism.

166. (New) A method of screening for DNA sequence variations in a population of individuals comprising:

providing a first nucleic acid sample from each of said individuals;

providing a second nucleic acid sample by fragmenting said first nucleic acid sample to produce fragments, denaturing said fragments, allowing some of said fragments to reanneal to form double stranded DNA sequences and removing said double stranded DNA sequences thus isolating said single stranded fragments;

providing a plurality of identical nucleic acid arrays wherein said arrays comprise probes which are designed to interrogate for DNA sequence variations;

hybridizing each of said second nucleic acid samples to one of said plurality of identical arrays; and

generating a plurality of hybridization patterns resulting from said hybridizations; and

analyzing the hybridization patterns to determine the presence or absence of sequence variation in the population of individuals.

167. (New) The method of claim 166 wherein said sequence variation is a single nucleotide polymorphism.

168. (New) A method of screening for DNA sequence variations in a population of individuals comprising:

providing a first nucleic acid sample from each of said individuals;

providing a second nucleic acid sample by amplifying said first nucleic acid sample by arbitrarily primed PCR to produce an amplification product and isolating said amplification product ;

providing a plurality of identical nucleic acid arrays wherein said arrays comprise probes which are designed to interrogate for DNA sequence variations;

hybridizing each of said second nucleic acid samples to one of said plurality of identical arrays; and

generating a plurality of hybridization patterns resulting from said hybridizations; and

analyzing the hybridization patterns to determine the presence or absence of sequence variation in the population of individuals.

A13

169. (New) The method of claim 168 wherein said sequence variation is a single nucleotide polymorphism.

170. (New) A method of screening for DNA sequence variations in a population of individuals comprising:

providing a first nucleic acid sample from each of said individuals;

providing a second nucleic acid sample by fragmenting said first nucleic acid sample to produce fragments, hybridizing said fragments to an oligonucleotide probe bound to a solid support, and isolating said hybridized fragments;

providing a plurality of identical nucleic acid arrays wherein said arrays comprise probes which are designed to interrogate for DNA sequence variations;

hybridizing each of said second nucleic acid samples to one of said plurality of identical arrays; and

generating a plurality of hybridization patterns resulting from said hybridizations; and

analyzing the hybridization patterns to determine the presence or absence of sequence variation in the population of individuals.

171. (New) The method of claim 170 wherein said sequence variation is a single nucleotide polymorphism.

172. (New) A method of screening for DNA sequence variations in a population of individuals comprising:

Attachment B: Canceled Claims:

1. (Canceled) A method of analyzing a first nucleic sample comprising:

providing said first nucleic acid sample;

reproducibly reducing the complexity of said first nucleic acid sample to produce a second nucleic acid sample which may comprise a plurality of non-identical sequences whereby said second nucleic acid sample is obtainable by:

fragmenting said first nucleic acid sample to produce fragments and ligating adaptor sequences to said fragments;

fragmenting said first nucleic acid sample to produce fragments, denaturing said fragments, allowing some of said fragments to reanneal to form double stranded DNA sequences and removing said double stranded DNA sequences.

amplification by arbitrarily primed PCR;

hybridizing said first nucleic acid sample to an oligonucleotide probe bound to a solid support;

hybridizing said first nucleic acid sequence to a mismatch binding protein;

providing a nucleic acid array;

hybridizing said second nucleic acid sample to said array; and

analyzing a hybridization pattern resulting from said hybridization.

2. (Canceled) The method of claim 1 wherein said second nucleic acid sample comprises at least 0.5 % of said nucleic acid sample

3. (Canceled) The method of claim 1 wherein said second nucleic acid sample comprises at least 3 % of said nucleic acid sample

4. (Canceled) The method of claim 1 wherein said second nucleic acid sample comprises at least 12 % of said nucleic acid sample
at least 12%

5. (Canceled) The method of claim 1 wherein said second nucleic acid sample comprises at least 50 % of said nucleic acid sample

6. (Canceled) The method of claim 1 wherein each of said non-identical sequences differs from the other non-identical sequences by at least 5 nucleic acid bases.

7. (Canceled) The method of claim 1 wherein each of said non-identical sequences differs from the other non-identical sequences by at least 10 nucleic acid bases.

8. (Canceled) The method of claim 1 wherein each of said non-identical sequences differs from the other non-identical sequences by at least 50 nucleic acid bases.

9. (Canceled) The method of claim 1 wherein each of said non-identical sequences differs from the other non-identical sequences by at least 1000 nucleic acid bases.

10. (Canceled) The method of claim 1 wherein said NA sample is DNA.

11. (Canceled) The method of claim 1 wherein said NA sample is genomic DNA.

12. (Canceled) The method of claim 1 wherein said first nucleic acid sample is cDNA derived from RNA or mRNA.

13. (Canceled) The method of claim 1 further comprising the step of amplifying at least one of the non-identical sequences in said second nucleic acid sample.

14. (Canceled) The method of claim 13 wherein said step of amplifying is performed by a polymerase chain reaction (PCR).

15. (Canceled) The method of claim 1 wherein the entire method is performed in a single reaction vessel.

16. (Canceled) The method of claim 1 wherein said step of fragmenting the first nucleic acid sample comprises digestion with at least one restriction enzyme.

17. (Canceled) The method of claim 1 wherein said step of fragmenting the first nucleic acid sample comprises digestion with a type IIs endonuclease.

18. (Canceled) The method of claim 1 wherein said adaptor sequences comprise PCR primer template sequences.

19. (Canceled) The method of claim 1 wherein said adaptor sequences comprise tag sequences.

20. (Canceled) The method of claim 1 wherein said solid support is a magnetic bead.

21. (Canceled) The method of claim 1 wherein said mismatch binding protein is bound to a magnetic bead.

22. (Canceled) The method of claim 1 wherein said method for analyzing a nucleic acid sample comprises determining whether the nucleic acid sample contains sequence variations.

23. (Canceled) The method of claim 22 wherein said sequence variations are single nucleotide polymorphisms.

24. (Canceled) The method of claim 1 wherein the step of obtaining a DNA array comprises:

designing a DNA array to query DNA fragments which have been produced by the identical procedures used to obtain said second nucleic acid sample.

25. (Canceled) The method of claim 24 wherein the step of designing further requires predetermining the sequences contained in said second nucleic acid sample.

26. (Canceled) The method of claim wherein said step of predetermining the sequences contained in said second nucleic acid sample is conducted in a computer system.

27. (Canceled) The method of claim 23 wherein said second nucleic acid sample is obtainable by:

binding oligonucleotide probes containing a desired SNP sequence to magnetic beads to form probe-bead complexes; and

hybridizing said probe-bead complexes to said DNA sample;

exposing said hybridized DNA sample to a single strand DNA nuclease to remove single stranded DNA thereby forming a DNA duplex;

ligating a double stranded adaptor sequence comprising a restriction enzyme site to said DNA duplex;

digesting said DNA duplex with a restriction enzyme to release the magnetic bead; and

isolating only those fragments containing said SNP sequence.

28. (Canceled) The method of claim 25 wherein said restriction enzyme is a Class IIs endonuclease.

29. (Canceled) The method of claim 23 wherein said second nucleic acid sample is obtainable by:

exposing the DNA sample to a mismatch bonding protein;

employing a 3' to 5' exonuclease to remove single stranded DNA; and

employing a nuclease to remove single stranded DNA.

30. (Canceled) A method of screening for DNA sequence variations in an individual comprising:

providing said first nucleic acid sample from said individual;

providing a second nucleic acid sample by reproducibly reducing the complexity of said first nucleic acid sample to produce a second nucleic acid sample which may comprise a plurality of non-identical sequences whereby said second nucleic acid sample is obtainable by:

fragmenting said first nucleic acid sample to produce fragments and ligating adaptor sequences to said fragments;

fragmenting said first nucleic acid sample to produce fragments, denaturing said fragments, allowing some of said fragments to reanneal to form double stranded DNA sequences and removing said double stranded DNA sequences.

amplification by arbitrarily primed PCR;

hybridizing said first nucleic acid sample to an oligonucleotide probe bound to a solid support;

hybridizing said first nucleic acid sequence to a mismatch binding protein;

providing a nucleic acid array;

hybridizing said second nucleic acid sample to said array; and

analyzing a hybridization pattern resulting from said hybridization.

31. (Canceled) The method of claim 30 wherein said sequence variation is a SNP.

32. (Canceled) The method of claim 31 wherein said SNP is associated with a disease.

33. (Canceled) The method of claim 31 wherein said SNP is associated with the efficacy of a drug.

34. (Canceled) A method of screening for DNA sequence variations in a population of individuals comprising:

providing said a first nucleic acid sample from each of said individuals;

providing a second nucleic acid sample by reproducibly reducing the complexity of said first nucleic acid sample to produce a second nucleic acid sample which may comprise a plurality of non-identical sequences whereby said second nucleic acid sample is obtainable by:

fragmenting said first nucleic acid sample to produce fragments and ligating adaptor sequences to said fragments;

fragmenting said first nucleic acid sample to produce fragments, denaturing said fragments, allowing some of said fragments to reanneal to form double stranded DNA sequences and removing said double stranded DNA sequences.

amplification by arbitrarily primed PCR;

hybridizing said first nucleic acid sample to an oligonucleotide probe bound to a solid support;

hybridizing said first nucleic acid sequence to a mismatch binding protein;

providing a nucleic acid array;

hybridizing said second nucleic acid sample to said array; and

analyzing a hybridization pattern resulting from said hybridization.

35. (Canceled) The method of claim 34 further comprising the step of compiling the analyses of each individual's hybridization pattern.

36. (Canceled) The method of claim 34 wherein said sequence variation is a SNP.

37. (Canceled) In a computer system, a method of designing an array comprising:
modeling specific enzymatic reactions between a known nucleic acid sequence and an enzyme;
obtaining the results of said modeled enzymatic reactions;
obtaining probe sequences based upon said results; and
designing an array to contain said probe sequences.